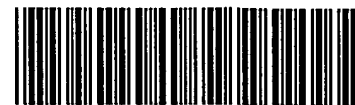


RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/567,749A
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TIME: 09:27:00

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3 <110> APPLICANT: Kruse, Daniela
4      Hertmann, Thomas
5      Thierbach, Georg
6      Rieping, Mechthild
9 <120> TITLE OF INVENTION: A Process for Preparing L-Threonione
11 <130> FILE REFERENCE: 7601/88025
13 <140> CURRENT APPLICATION NUMBER: 10/567749A
14 <141> CURRENT FILING DATE: 2006-02-10
16 <160> NUMBER OF SEQ ID NOS: 10
18 <170> SOFTWARE: PatentIn version 3.4
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21 <211> LENGTH: 993
22 <212> TYPE: DNA
23 <213> ORGANISM: Escherichia coli
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35 ttt gat gag aac gga gtt gag gtt ttt gac gaa aag gcc tta gta gaa      96
36 Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu
37          20          25          30
39 cag gaa ccc agt gat aac gat ttg gcc gaa gag gaa ctg tta tcg cag      144
40 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln
41          35          40          45
43 gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag      192
44 Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
45          50          55          60
47 att ggt tat tca cca ctg tta acg gcc gaa gaa gaa gtt tat ttt gcg      240
48 Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala
49 65          70          75          80
51 cgt cgc gca ctg cgt gga gat gtc gcc tct cgc cgc cgg atg atc gag      288
52 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
53          85          90          95
55 agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt      336
56 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
57          100          105          110
59 ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc      384
60 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
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63 cgc gcg gta gag aag ttt gac ccg gaa cgt ggt ttc cgc ttc tca aca      432
64 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
65      130      135      140
67 tac gca acc tgg tgg att cgc cag acg att gaa cgg gcg att atg aac      480
68 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
69 145      150      155      160
71 caa acc cgt act att cgt ttg ccg att cac atc gta aag gag ctg aac      528
72 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
73      165      170      175
75 gtt tac ctg cga acc gca cgt gag ttg tcc cat aag ctg gac cat gaa      576
76 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
77      180      185      190
79 cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac      624
80 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
81      195      200      205
83 gtc agc cgt atg ctt cgt ctt aac gag cgc att acc tcg gta gac acc      672
84 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
85      210      215      220
87 ccg ctg ggt ggt gat tcc gaa aaa gcg ttg ctg gac atc ctg gcc gat      720
88 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
89 225      230      235      240
91 gaa aaa gag aac ggt ccg gaa gat acc acg caa gat gac gat atg aag      768
92 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
93      245      250      255
95 cag agc atc gtc aaa tgg ctg ttc gag ctg aac gcc aaa cag cgt gaa      816
96 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
97      260      265      270
99 gtg ctg gca cgt cga ttc ggt ttg ctg ggg tac gaa gcg gca aca ctg      864
100 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
101      275      280      285
103 gaa gat gta ggt cgt gaa att ggc ctc acc cgt gaa cgt gtt cgc cag      912
104 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
105      290      295      300
107 att cag gtt gaa ggc ctg cgc cgt ttg cgc gaa atc ctg caa acg cag      960
108 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
109 305      310      315      320
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126      20      25      30
128 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln

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Output Set: N:\CRF4\12282006\J567749A.raw

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132          50          55          60
134 Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala
135 65          70          75          80
137 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
138          85          90          95
140 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
141          100          105          110
143 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
144          115          120          125
146 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
147          130          135          140
149 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
150 145          150          155          160
152 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
153          165          170          175
155 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
156          180          185          190
158 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
159          195          200          205
161 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
162          210          215          220
164 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
165 225          230          235          240
167 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
168          245          250          255
170 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
171          260          265          270
173 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
174          275          280          285
176 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
177          290          295          300
179 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
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183          325          330
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192 <221> NAME/KEY: Allele
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194 <223> OTHER INFORMATION: rpoS allele
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199 <223> OTHER INFORMATION: amber codon

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206 gccgaagagg aactgttatc gcagggagcc acacagcgtg tgttggaagc gactcagctt      180
208 taccttggtg agattgggta ttcaccactg ttaacggccg aagaagaagt ttattttgcg      240
210 cgtcgcgcac tgcgtggaga tgcgcctct cgccgccgga tgatcgagag taacttgcgt      300
212 ctggtggtaa aaattgcccg ccgttatggc aatcgtggtc tggcgttgct ggaccttacc      360
214 gaagagggca acctggggct gatccgcgcg gtagagaagt ttgaccgga acgtggtttc      420
216 cgcttctcaa catacgcaac ctggtggatt cgccagacga ttgaacgggc gattatgaac      480
218 caaaccgta ctattcgttt gccgattcac atcgtaaagg agctgaacgt ttacctgcga      540
220 accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaga gatcgagag      600
222 caactggata agccagttga tgacgtcagc cgtatgcttc gtcttaacga gcgcattacc      660
224 tcggtagaca ccccgctggg tgggtgattcc gaaaaagcgt tgctggacat cctggccgat      720
226 gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc      780
228 aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg      840
230 ctggggtagc aagcggcaac actggaagat gtaggtcgtg aaattggcct caccgctgaa      900
232 cgtgttcgcc agattcaggt tgaaggcctg cgccgtttgc gcgaaatcct gcaaacgcag      960
234 gggctgaata tcgaagcgct gttccgcgag taa                                993
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238 <211> LENGTH: 75
239 <212> TYPE: DNA
240 <213> ORGANISM: Escherichia coli
242 <220> FEATURE:
243 <221> NAME/KEY: tRNA
244 <222> LOCATION: (1)..(75)
245 <223> OTHER INFORMATION: supE allele
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255 <211> LENGTH: 1545
256 <212> TYPE: DNA
257 <213> ORGANISM: Escherichia coli
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262 <223> OTHER INFORMATION: ilvA-Gen
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267 1          5          10          15
269 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg      96
270 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
271          20          25          30
273 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att      144
274 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
275          35          40          45
277 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc      192
278 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg

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282	Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His			
283	65 70 75 80			
285	ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt	288		
286	Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe			
287	85 90 95			
289	tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc	336		
290	Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala			
291	100 105 110			
293	acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg	384		
294	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val			
295	115 120 125			
297	ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa	432		
298	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu			
299	130 135 140			
301	ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg	480		
302	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro			
303	145 150 155 160			
305	atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag	528		
306	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln			
307	165 170 175			
309	gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg	576		
310	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu			
311	180 185 190			
313	gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa	624		
314	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys			
315	195 200 205			
317	gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg	672		
318	Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu			
319	210 215 220			
321	gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa	720		
322	Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu			
323	225 230 235 240			
325	ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag	768		
326	Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln			
327	245 250 255			
329	gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg	816		
330	Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala			
331	260 265 270			
333	gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg gaa ccc tct	864		
334	Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser			
335	275 280 285			
337	ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac	912		
338	Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn			
339	290 295 300			
341	att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac	960		
342	Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn			
343	305 310 315 320			

VERIFICATION SUMMARY

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